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AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph that begins on page 8, line 25 with the following re-written paragraph:

FIGURE 6A is a schematic representation of the peptide display library depicting the insertion point for 45-base oligonucleotides (SEQ ID NO: 1) of the composition $(NNG/C/T)_{15}$ (N = any base), which encode randomized 15-amino acid peptides inserted in frame within GFP.

Please replace the paragraph that begins on page 82, line 3 with the following re-written paragraph:

Methods. The constructs employed for the generation of the peptide display library are depicted in FIGURE 6A. In brief, 45-residue oligonucleotides (SEQ ID NO: 1) of the composition $(NNG/T/C)_{15}$ were inserted into pVT21 using XhoI and BamHI restriction enzyme sites ~~which~~ that had previously been engineered into the green fluorescent protein (GFP) at nucleotide position 468. The yeast genomic fragment library was constructed by digesting genomic DNA from strain yVT5 (MATa, leu2-3, 112, trp1-1, ura3-1, his3-11, 15, ade2-1, can1-100 [strain JRY2334] with DpnII (New England Biolabs, Beverly, MA), isolating digested DNA 100-500 base pairs in length from a 1% agarose gel using the gene clean 111 kit (BIO 101), and ligating the purified DNA to pVT21 that had previously been digested with BglII (New England Biolabs, Beverly, MA), treated with calf intestinal phosphatase (New England Biolabs, Beverly, MA), and purified. Following ligation, DNA was introduced into *E. coli* strain DH5-α by electroporation, and the resulting amplified library purified using the Qiagen "maxi-prep" kit (~~Quiagen~~ Qiagen, Valencia, CA; Hilden, Germany).

Please replace the paragraph that begins on page 86, line 13 with the following re-written paragraph:

PCR Amplification And Sequencing Of Library Clone DNA. Whole-colony PCR was performed by transferring yeast cells from single colonies to PCR vessels, microwaving the cells for one minute at full power, and immediately cooling the cells on ice. After cooling, PCR reactions were performed using standard reagents and protocols. Ausubel *et al.*, (eds.) *Current*

Protocols in Molecular Biology, John Wiley and Sons, New York (1996). Primers used to amplify the genomic inserts were oVT201 (5'-ATT TTA GCG TAA AGG ATG GGG-3') (SEQ ID NO: 2), which is homologous to a region within the PGK1 3' untranslated region (3'UTR), and oVT326 (5'-TGA GAA TTC GGA TCC AAG AGA GAC CAC ATG GTC C-3') (SEQ ID NO: 3), part of which is homologous to a region within the GFP coding region. Sequencing of the 5' and 3' ends of genomic inserts present in both PCR-amplified products and plasmid DNA was accomplished with primers oVT326 and oVT201, and sequence data was obtained using an ABI373A DNA sequencer (Applied Biosystems Division, Perkin-Elmer, Inc., Foster City, CA).

Please replace the paragraph that begins on page 88, line 19 with the following re-written paragraph:

In the following Example, perturbagens are used to explore the biochemical mechanisms underlying the establishment of a productive adenovirus infection in human embryonic kidney cells. Growth-proficient host cells are identified by positive selection for growth, and also by selection based on fluorescence. Although in this Example adenovirus is utilized, one ~~ofordinary~~ of ordinary skill will appreciate that the methodology is equally applicable to HIV and to other viruses.

Please replace the paragraph that begins on page 89, line 9 with the following re-written paragraph:

Alternatively, a cDNA library of, e.g., 13 or 16 x 10^6 clones is cloned into the C-terminus of dead GFP, using standard methods. The library cDNA encoding human protein domains was prepared, using methods that are well known in the art, from human placental tissue. Poly(A)RNA is isolated from placental tissue by standard methods. First strand cDNA is then generated from poly(A)+ mRNA using a primer containing a random 9-mer, a SfiI restriction endonuclease site and a site for PCR amplification (SEQ ID NO: 4) (5'-ACTCTGGACTAGGCAGGTTCAGTGGCCATTATGGCCNNNNNNNNN). The second strand is then generated using a primer consisting of a random 6-mer, another SfiI site, and a site for PCR amplification (SEQ ID NO: 5)

(5'-AAGCAGTGGTGTCAACGCAGTGAGGCCGAGGCGGCCNNNNNN). After conducting a number of PCR amplification cycles, the DNA is cut with SfiI and the resultant fragments are size-selected for fragments of greater than about 4000 bp. The selected fragments are ligated into the SfiI sites of a suitable expression vector, as described herein. Such libraries were introduced into *E. coli*, packaged and transduced into 293 cells as described above.

Please append the enclosed paper copy of the sequence listing to the end of the specification. The sequence listing is a copy from parent application 09/259,155, relied upon for priority in the present application.